

SEQUENCE LISTING

<110> Kihara Memorial Yokohama Foundation for the Advancement of Life Sciences
City of Yokohama

<120> TRF2 DNA-binding domain mutant proteins, telomeric DNA mutants, and use
of a
structure of a complex between a TRF2 DNA binding domain and a double-stranded
DNA molecule

<130> FP-047PCT

<140> 10/590,464

<141> 2006-08-23

<150> JP P2004-046238

<151> 2004-02-23

<160> 29

<170> PatentIn version 3.1

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<213> Homo sapiens

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<221> CDS

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gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac	96
Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn	
20 25 30	

tgg gct gcc att tct aaa aat tac cca ttt gtt aac cga aca gct gtg	144
Trp Ala Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ala Val	
35 40 45	

atg att aag gat cgc tgg cgg acc atg aaa aga ctt ggc atg aac	189
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Met Ile Lys Asp Arg Trp Arg Thr Met Lys Arg Leu Gly Met Asn
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 gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac 96
 Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn
 20 25 30
 tgg gct gcc att tct aaa aat tac cca ttt gtt aac cga aca gct gtg 144
 Trp Ala Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ala Val
 35 40 45
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Met Ile Lys Asp Arg Trp Arg Thr Met Lys Arg Leu Gly Met Asn
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 <223> Mutant A471S of hTRF2-DBD

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gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac 96
 Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn
 20 25 30

tgg tct gcc att tct aaa aat tac cca ttt gtt aac cga aca gct gtg 144
 Trp Ser Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ala Val
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Met Ile Lys Asp Arg Trp Arg Thr Met Lys Arg Leu Gly Met Asn
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 <223> Mutant A484S of hTRF2-DBD

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gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac 96
 Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn
 20 25 30

tgg gct gcc att tct aaa aat tac cca ttt gtt aac cga aca tct gtg 144
 Trp Ala Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ser Val
 35 40 45

atg att aag gat cgc tgg cgg acc atg aaa aga ctt ggc atg aac 189
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Met Ile Lys Asp Arg Trp Arg Thr Met Lys Arg Leu Gly Met Asn
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 gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac 96
 Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn
 20 25 30
 tgg gct gcc att tct aaa aat tac cca ttt gtt aac cga aca gct gtg 144
 Trp Ala Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ala Val
 35 40 45
 atg att aag gat cgc tgg cgg acc atg aaa aag ctt ggc atg aac 189
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Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn
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Trp Ala Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ala Val
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Met Ile Lys Asp Arg Trp Arg Thr Met Lys Lys Leu Gly Met Asn
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 gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac 96
 Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn
 20 25 30
 tgg tct gcc att tct aaa aat tac cca ttt gtt aac cga aca tct gtg 144
 Trp Ser Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ser Val
 35 40 45
 atg att aag gat cgc tgg cgg acc atg aaa aag ctt ggc atg aac 189
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Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn
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 35 40 45

Met Ile Lys Asp Arg Trp Arg Thr Met Lys Lys Leu Gly Met Asn
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 1 5 10 15

gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac 96
 Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn
 20 25 30

tgg tct gcc att tct aaa aat tac cca ttt gtt aac cga aca tct gtg 144
 Trp Ser Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ser Val
 35 40 45

atg att aag gat cgc tgg cgg acc atg aaa aga ctt ggc atg aac 189
 Met Ile Lys Asp Arg Trp Arg Thr Met Lys Arg Leu Gly Met Asn
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1				5					10					15			
agg	cgg	gcg	tcc	cgc	agt	agc	ggg	cgg	gcc	cgg	cgg	ggg	cgc	cac	gag		96
Arg	Arg	Ala	Ser	Arg	Ser	Ser	Gly	Arg	Ala	Arg	Arg	Gly	Arg	His	Glu		
			20					25					30				
ccg	ggg	ctg	ggg	ggc	ccg	gcg	gag	cgc	ggc	gcg	ggg	gag	gca	cgg	ctg		144
Pro	Gly	Leu	Gly	Gly	Pro	Ala	Glu	Arg	Gly	Ala	Gly	Glu	Ala	Arg	Leu		
		35					40					45					
gaa	gag	gca	gtc	aat	cgc	tgg	gtg	ctc	aag	ttc	tac	ttc	cac	gag	gcg		192
Glu	Glu	Ala	Val	Asn	Arg	Trp	Val	Leu	Lys	Phe	Tyr	Phe	His	Glu	Ala		
	50					55					60						
ctg	cgg	gcc	ttt	cgg	ggt	agc	cgg	tac	ggg	gac	ttc	aga	cag	atc	cgg		240
Leu	Arg	Ala	Phe	Arg	Gly	Ser	Arg	Tyr	Gly	Asp	Phe	Arg	Gln	Ile	Arg		
65					70					75				80			
gac	atc	atg	cag	gct	ttg	ctt	gtc	agg	ccc	ttg	ggg	aag	gag	cac	acc		288
Asp	Ile	Met	Gln	Ala	Leu	Leu	Val	Arg	Pro	Leu	Gly	Lys	Glu	His	Thr		
			85					90					95				
gtg	tcc	cga	ttg	ctg	cgg	gtt	atg	cag	tgt	ctg	tcg	cgg	att	gaa	gaa		336
Val	Ser	Arg	Leu	Leu	Arg	Val	Met	Gln	Cys	Leu	Ser	Arg	Ile	Glu	Glu		
			100					105					110				
ggg	gaa	aat	tta	gac	tgt	tcc	ttt	gat	atg	gag	gct	gag	ctc	aca	cca		384
Gly	Glu	Asn	Leu	Asp	Cys	Ser	Phe	Asp	Met	Glu	Ala	Glu	Leu	Thr	Pro		

115	120	125	
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Leu Glu Ser Ala Ile Asn Val	Leu Glu Met Ile Lys Thr Glu Phe Thr		
130	135 140		
ctg aca gaa gca gtg gtc gaa tcc agt aga aaa ctg gtc aag gaa gct		480	
Leu Thr Glu Ala Val Val Glu Ser Ser Arg Lys Leu Val Lys Glu Ala			
145	150 155 160		
gct gtc att att tgt atc aaa aac aaa gaa ttt gaa aag gct tca aaa		528	
Ala Val Ile Ile Cys Ile Lys Asn Lys Glu Phe Glu Lys Ala Ser Lys			
	165 170 175		
att ttg aaa aaa cat atg tcc aag gac ccc aca act cag aag ctg aga		576	
Ile Leu Lys Lys His Met Ser Lys Asp Pro Thr Thr Gln Lys Leu Arg			
	180 185 190		
aat gat ctc ctg aat att att cga gaa aag aac ttg gcc cat cct gtt		624	
Asn Asp Leu Leu Asn Ile Ile Arg Glu Lys Asn Leu Ala His Pro Val			
	195 200 205		
atc cag aac ttt tca tat gag acc ttc cag cag aag atg ctg cgc ttc		672	
Ile Gln Asn Phe Ser Tyr Glu Thr Phe Gln Gln Lys Met Leu Arg Phe			
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ctg gag agc cac ctg gat gac gcc gag ccc tac ctc ctc acg atg gcc		720	
Leu Glu Ser His Leu Asp Asp Ala Glu Pro Tyr Leu Leu Thr Met Ala			
225	230 235 240		
aaa aag gct ttg aaa tct gag tcc gct gcc tca agt aca ggg aag gaa		768	
Lys Lys Ala Leu Lys Ser Glu Ser Ala Ala Ser Ser Thr Gly Lys Glu			
	245 250 255		
gat aaa cag cca gca cca ggg cct gtg gaa aag cca ccc aga gaa ccc		816	
Asp Lys Gln Pro Ala Pro Gly Pro Val Glu Lys Pro Pro Arg Glu Pro			
	260 265 270		
gca agg cag cta cgg aat cct cca acc acc att gga atg atg act ctg		864	
Ala Arg Gln Leu Arg Asn Pro Pro Thr Thr Ile Gly Met Met Thr Leu			
	275 280 285		
aaa gca gct ttc aag act ctg tct ggt gca cag gat tct gag gca gcc		912	
Lys Ala Ala Phe Lys Thr Leu Ser Gly Ala Gln Asp Ser Glu Ala Ala			
	290 295 300		
ttt gca aaa ctg gac cag aag gat ctg gtt ctt cct act caa gct ctc		960	
Phe Ala Lys Leu Asp Gln Lys Asp Leu Val Leu Pro Thr Gln Ala Leu			
305	310 315 320		
cca gca tca cca gcc ctc aaa aac aag aga ccc aga aaa gat gaa aac		1008	
Pro Ala Ser Pro Ala Leu Lys Asn Lys Arg Pro Arg Lys Asp Glu Asn			
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Glu Ser Ser Ala Pro Ala Asp Gly Glu Gly Gly Ser Glu Gln Pro			
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cag agt act gag ccc agc gca ggc ctc aac tcc tcc cag gag gcc gct Gln Ser Thr Glu Pro Ser Ala Gly Leu Asn Ser Ser Gln Glu Ala Ala 370 375 380	1152
tca gcg cca cca tcc aag ccc acc gtt ctc aac caa ccc ctc cct gga Ser Ala Pro Pro Ser Lys Pro Thr Val Leu Asn Gln Pro Leu Pro Gly 385 390 395 400	1200
gag aag aat ccc aaa gta ccc aaa ggc aag tgg aac agc tct aat ggg Glu Lys Asn Pro Lys Val Pro Lys Gly Lys Trp Asn Ser Ser Asn Gly 405 410 415	1248
gtt gaa gaa aag gag act tgg gtg gaa gag gat gaa ctg ttt caa gtt Val Glu Glu Lys Glu Thr Trp Val Glu Glu Asp Glu Leu Phe Gln Val 420 425 430	1296
cag gca gca cca gat gaa gac agt aca acc aat ata aca aaa aag cag Gln Ala Ala Pro Asp Glu Asp Ser Thr Thr Asn Ile Thr Lys Lys Gln 435 440 445	1344
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35 40 45

Glu Glu Ala Val Asn Arg Trp Val Leu Lys Phe Tyr Phe His Glu Ala
50 55 60

Leu Arg Ala Phe Arg Gly Ser Arg Tyr Gly Asp Phe Arg Gln Ile Arg
65 70 75 80

Asp Ile Met Gln Ala Leu Leu Val Arg Pro Leu Gly Lys Glu His Thr
85 90 95

Val Ser Arg Leu Leu Arg Val Met Gln Cys Leu Ser Arg Ile Glu Glu
100 105 110

Gly Glu Asn Leu Asp Cys Ser Phe Asp Met Glu Ala Glu Leu Thr Pro
115 120 125

Leu Glu Ser Ala Ile Asn Val Leu Glu Met Ile Lys Thr Glu Phe Thr
130 135 140

Leu Thr Glu Ala Val Val Glu Ser Ser Arg Lys Leu Val Lys Glu Ala
145 150 155 160

Ala Val Ile Ile Cys Ile Lys Asn Lys Glu Phe Glu Lys Ala Ser Lys
165 170 175

Ile Leu Lys Lys His Met Ser Lys Asp Pro Thr Thr Gln Lys Leu Arg
180 185 190

Asn Asp Leu Leu Asn Ile Ile Arg Glu Lys Asn Leu Ala His Pro Val
195 200 205

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Leu Glu Ser His Leu Asp Asp Ala Glu Pro Tyr Leu Leu Thr Met Ala
225 230 235 240

Lys Lys Ala Leu Lys Ser Glu Ser Ala Ala Ser Ser Thr Gly Lys Glu
245 250 255

Asp Lys Gln Pro Ala Pro Gly Pro Val Glu Lys Pro Pro Arg Glu Pro

260

265

270

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Lys Ala Ala Phe Lys Thr Leu Ser Gly Ala Gln Asp Ser Glu Ala Ala
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Phe Ala Lys Leu Asp Gln Lys Asp Leu Val Leu Pro Thr Gln Ala Leu
 305 310 315 320

Pro Ala Ser Pro Ala Leu Lys Asn Lys Arg Pro Arg Lys Asp Glu Asn
 325 330 335

Glu Ser Ser Ala Pro Ala Asp Gly Glu Gly Gly Ser Glu Leu Gln Pro
 340 345 350

Lys Asn Lys Arg Met Thr Ile Ser Arg Leu Val Leu Glu Glu Asp Ser
 355 360 365

Gln Ser Thr Glu Pro Ser Ala Gly Leu Asn Ser Ser Gln Glu Ala Ala
 370 375 380

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Glu Lys Asn Pro Lys Val Pro Lys Gly Lys Trp Asn Ser Ser Asn Gly
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Val Glu Glu Lys Glu Thr Trp Val Glu Glu Asp Glu Leu Phe Gln Val
 420 425 430

Gln Ala Ala Pro Asp Glu Asp Ser Thr Thr Asn Ile Thr Lys Lys Gln
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Lys Trp Thr Val Glu Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys
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Tyr Gly Glu Gly Asn Trp Ala Ala Ile Ser Lys Asn Tyr Pro Phe Val
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